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BY	CLASS
	SUBCLASS
	DRAFTSMAN

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	CLASS	
DRAFTSMAN	BY	

751	CTGCCAGTGGCCCTTGGGGGACGGCGACTCAGTGCTGAGGCCTCACCTTCGGCAGCTTGAACCTTGACCTTGACCTTGCGCTCCTG	C	Q	W	A	L	R	G	D	A	D	S	V	L	S	L	T	F	R	S	F	D	L	A	S	C	268
826	CGACCGAGGGCGAGGGACCTGGTGTGACGGTGTACACACCCATGGAGCCCCACAGGCCCTGAGGCCCATGGAGCCCCACAGGCCCTGGAGCACTT	D	E	R	G	S	D	L	V	T	V	Y	N	T	L	S	P	M	E	P	H	A	L	V	Q	L	293
901	GTGGCACCTACCCCTCCCTAACAAACCTGACCTTCCACTCCAGAACGTTCTGGCTCATCACACTGATAAC	C	G	T	Y	P	P	S	Y	N	L	T	F	H	S	S	Q	N	V	L	L	I	T	L	I	T	318
976	CAACACTGAGGGGGCATCCGGGTTGAGGCCACCTTCCAGCTGCCTAGGATGAGCAGGCTGTGGAGGGCCG	N	T	E	F	F	H	P	G	F	E	A	T	F	F	Q	L	P	R	M	S	S	C	G	G	R	343
1051	CTTACGTAAGCCCAGGGACATTCAACAGGCCCTACTACCCAGGCCACTACCCAAACATGACTGCACATG	L	R	K	A	Q	G	T	F	N	S	P	Y	P	G	H	Y	P	P	N	I	D	C	T	W	368	
1126	GAACATGAGGTGGCCAACAAACAGCATGTGAAGGTGAGCTTCAAAATTCTTCTACCTGCTGGAGCCCCGGCGTGCCT	N	I	E	V	P	N	N	Q	H	V	K	V	S	F	K	F	F	Y	L	L	E	P	G	V	P	393
1201	TGGGGCACCTGGCAAGGACTACGTGGAGATCAATGGGAGAAATACTGGGAGAGGTTCCCAAGTTCGTCGTT	A	G	T	C	P	K	D	Y	V	E	I	N	G	E	K	Y	C	G	E	R	S	Q	F	V	418	
1276	CACCAGCAACAGCAACAAGATCACAGTTGGCTTCCACTCAGATCACCTGCTTACACGGACACCGGCTCTTAGCTGA	T	S	N	S	N	K	I	T	V	R	F	H	S	D	Q	S	Y	T	D	T	G	F	L	A	E	443
1351	ATACACCTCTTACGACTCCAGTGAACCCATGCCGGCATGGGGCAGTTCACGTGCGCACGGGGGTATCCGGAAAGCA	Y	L	S	Y	D	S	S	D	P	C	P	G	Q	F	T	C	R	T	G	R	C	I	R	K	E	468
1426	GCTGGCTGTGATGGCTGGGACTGACGGACCAAGGCCACTGGCACTGGCAGTTGCGACGGCCGGCCACCA	I	B	C	D	G	W	A	D	C	T	D	H	S	D	E	L	N	C	S	C	D	A	G	H	Q	493

Fig. 2B

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1501 GTTCACGTGCAAGAACAAAGTCTGCAAGCCCCCTTCTGGGTCTGGGACTGGTGAACAGTGCAGCTGGGAGACAACAG
F T C K N K F C K P L F W V C D S V N D C G D N S 518

1576 CGACGAGCAGGGTGCAGTTGTCGGCCAGACCTTCAGGTGTTCCAATGGAAAGTGCCTCTCGAAAAGGCCAGCA
D E Q G C S C P A Q T F R C S N G K C L S K S Q Q 543

1651 GTGCAATGGAAAGGACGACTGTGGGACGGGCTCTGCCAAGGGTGAACCGTGTCACTTGTAC
C N G K D D C G D S D E A S C P K V N V V T C T 568

1726 CAAACACACTAACCGCTGCCTCAATGGCTCTGAGCAAGGGCAACCCCTGAGTGTGACGGGAAGGGGACTG
K H T Y R C L N G L C L S K G N P E C D G K E D C 593

1801 TAGCGACGGCTCAGATGAGAAGGACTGGGACTGTGGCTGGGTCACTCACGAGACAGGCTCGTGTGGGGG
S D G S D E K D C D C G L R S F T R Q A R V V G G 618

1876 CACGGATGGGATGAGGGGAGTGGGGCTGGCAGGTAAGCCTGCATGCTCTGGGCCAGGGCACATCTGGGTGC
T D A D E G E W P W Q V S L H A L G Q G H I C G A 643

1951 TTCCCTCATCTCTGGCTGGTCTGCCGACACTGGCTACATCGATGACAGAGGATTCAAGGTACTCAGA
S L I S P N W L V S A A H C Y I D D R G F R Y S D 668

2026 CCCCACGGCAGGGCTTCCCTGGGCTTGACGACCAAGGCCAGGGCAGGGCAGGGCCCTGGGTGCAGGGGGCAG
P T Q W T A F L G L H D Q S Q R S A P G V Q E R R 693

2101 GCTCAAGGGCATCATCTCCCACCCCTTCAATGACTTCACCTTGACTATGACATGGGCTGCTGGAGGTGGA
L K R I I S H P F N D F T F D Y D I A L L E L E 718

2176 GAAACCAGGAGACTACAGCTCCATGGTGGGCCATCTGGCTGCCACTGGCTTCCCATGCTTCCCTGGCGCAA
K P A E Y S S M V R P I C L P D A S H V F P A G K 743

Fig. 2C

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2251 GGCCATCTGGTCA CGGGC ACTGGAGGACACCCAGTATGGAGGC ACTGGCGGCTGATCCTGC AAAAGGGTGAGAT
 A I W V T G W G H T Q Y G G T G A L I L Q K G E I 768
 2326 CCGCGTCATCAA ACCAGACCCTGCCAGAAACTCCTGCCAGCATCACGCCCGCGCATGATGTGGCTGGCTT
 R V I N Q T T C E N L L P Q Q I T P R M M C V G F 793
 2401 CCTCAGCGGGCGTGGACTCCTGCCAGGGTGA TTCCGGGGACCCCTGTCCAGCGTGGAGGGGATGGGGAT
 L S G G V D S C Q G D S G G P L S S V E A D G R I 818
 2476 CTTCCAGGGCCGGTGTGGTGA GGAGACGGCTGGCTCAAGAGGAACAAGCCAGGGCTGTACACAAGGCTCCC
 F Q A F C C S W G D G C A Q R N K P G V Y T R L P 843
 2551 TCTGTTCGGGACTGGATCAAAGAGAACACTGGGTATAAGGGGTAGGGCCACCCAAATGTGTACACCTGGGGGG
 L F R D W I K E N T G V (SEQ ID NO: 2) 855
 2626 CCACCCATCGTCCACCCCAAGTGTGCACGCCCTGCAGGCTTCAATCTCCAGGGCTCCAATCTGCCTAGAAACCTCTCGCTTCAGCCTCCAAAGTGC
 2701 CATAACACTGTGA ACTCAATCTCCAGGGCTTCAACTGACCCAAACTGGCAACTGGTTCTACTGACCCAAACTGGCAAAAGTTGAAGACACAGCCT
 2776 AGCTGGGAGGTAGAAGGGGAGACACTGGTGGTTCTACTGACCCAACTGGCAACTGGCTTCTGCTGCTCCCTGTCTGTAAAGGAGCAGGGAA
 2851 CCCCGCCAGCCCCAAGCTGGCCGGCGCTTGTGTATACTCTGCTCTCCCTGTCTGTAAAGGAGCAGGGAA
 2926 CGGAGCTCGGAGGCCTCAGTGAAGGGTGGTGGGGCTGCCGATCTGGGGCTGTGGCCACGGCTCT
 3001 TGAGGAAGCCCAGGGCTCGGAGGCCCTGGAAACAGACGGGTCTGAGACTGAAATTGTGTTACCAAGCTCCAGGG
 3076 TGGACTTCAGTGTGTATTGTGTAAATGGTAAACAATTATTCTTTAAAAAAA (SEQ ID NO: 1)

- : KOZAK'S CONSENSUS SEQUENCE
- : TRANSMEMBRANE DOMAIN
- : CONSERVED AMINO ACIDS OF CATALYTIC TRIAD H,D,S

Fig. 2D

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